

Run on:	August 27, 2003, 00:25:23 ; Search time 40 Seconds	Perfect score: 327	US-09-541-462B-1
Scoring table:	IDENTITY_NUC	Sequence: 1 atggcgccagcgatggatgt.....tccaaaaggatg9gcactag	327
		Gapext: Gapext 1.0	
Searched:	569378 seqs, 220691566 residues	Total number of hits satisfying chosen parameters:	1139956
Minimum DB seq length:	0	Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%	Maximum Match 100%	Listing first 45 summaries
Database :	Issued_Patents_NA: * 1: /cgn2_6/pctodata/2/inav/5A_COMB.seq: * 2: /cgn2_6/pctodata/2/inav/5B_COMB.seq: * 3: /cgn2_6/pctodata/2/inav/6A_COMB.seq: * 4: /cgn2_6/pctodata/2/inav/6B_COMB.seq: * 5: /cgn2_6/pctodata/2/inav/6C_COMB.seq: * 6: /cgn2_6/pctodata/2/inav/backfile1.seq: *		
Pred. NO.	1	No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES			
Result No.	Score	Query Length	DB ID
1	253.6	77.6	3208
2	90	27.5	301
3	31	9.5	2408
4	31	9.5	2408
5	31	9.5	2408
6	31	9.5	2408
7	30	9.5	2408
8	29.2	8.9	2951
9	29.2	8.9	2951
10	28.6	8.7	648
11	28.6	8.7	723
12	28.6	8.7	1080
13	28.6	8.7	1080
14	28.6	8.7	1080
15	28.6	8.7	1488
16	28.6	8.7	2518
17	28.4	8.7	3420
18	28.4	8.7	3420
19	28.4	8.7	1
20	28.4	8.7	4707
21	28.4	8.7	4707
22	28.4	8.7	4707
23	28.4	8.7	35524
24	28.2	8.6	31880
c	25	8.6	42831
c	26	8.4	903
c	27	8.4	70000

RESULT 1	US-09-780-016-27
;	Sequence 27, Application US/09780016
;	Patent No. 6509456
;	GENERAL INFORMATION:
;	APPLICANT: Donoho, Gregory
;	APPLICANT: Scoville, John
;	APPLICANT: Turner, C. Alexander Jr.
;	APPLICANT: Friedrich, Glenn
;	APPLICANT: Abulin, Alejandro
;	APPLICANT: Zambrowicz, Brian
;	APPLICANT: Sands, Arthur T.
;	TIME OF INVENTION: 1
;	TITLE OF INVENTION: Polynucleotides Encoding the Same
;	FILE REFERENCE: LEX-0132-USA
;	CURRENT APPLICATION NUMBER: US/09-780,016
;	CURRENT FILING DATE: 2001-02-09
;	PRIOR APPLICATION NUMBER: US 60/181,294
;	PRIOR FILING DATE: 2000-02-11
;	NUMBER OF SEQ ID NOS: 27
;	SOFTWARE: FastSEQ for Windows Version 4.0
;	SEQ ID NO 27
;	LENGTH: 3208
;	TYPE: DNA
;	ORGANISM: homo sapiens
;	US-09-780-016-27
;	Query Match 77.6%; Score 253.6; DB 4; Length 3208;
;	Best Local Similarity 98.5%; Pred. No. 4.2e-78;
;	Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;	Sequence 1, Appl1
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Sequence 93. Appl1
Sequence 94. Appl1
Sequence 95. Appl1
Sequence 96. Appl1
Sequence 97. Appl1
Sequence 98. Appl1
Sequence 99. Appl1
Sequence 100. Appl1

RESULT 2
US-09-313-294A-492
Sequence 492, Application US/09313294A
; Patient No. 6476212
GENERAL INFORMATION:
; APPLICANT: Laigudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 492
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549333H1
US-09-313-294A-492

Query Match 27.5%; Score 90; DB 4; Length 301;
Best Local Similarity 74.0%; Pred. No. 1.2e-21; Matches 114; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 38 CCAACAGGGGGGGGAGAAGCGCTTGAAGTGAAAGTGAGTCAGAGAGGGCTAGTGCCCT 97
Db 146 CCGCTCCCGCAGGCCAACAGCGCTTGAGATCAGAGAGGGACCCGTGCGCT 205
QY 98 GGGCTGGATATGTTGTTGAACTTGCCATCTGGAGAACCATATGGATCTTT 157
Db 206 GGCGATGGATATGTCCTCGAGAACCTGCGCTATCGGCACACCATACTGGATCT 265
QY 158 GCATAGAAATGTCAGTACACAGGGCTCGCTAC 191
Db 266 GCATCGAGTGGCCAGGGCACACAGCGGAC 299

RESULT 3
US-08-608-241-1
Sequence 1, Application US/08608241
; General Information:
; APPLICANT: Donohue, Timothy J
; APPLICANT: Barber, Robert D
; APPLICANT: Wittuhn, Vernon
; TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/08/608,241
; FILING DATE: 08/08/608,241
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296,93511

RESULT 4
US-08-922-182-1
Sequence 1, Application US/08922182
; General Information:
; Patient No. 5834300
GENERAL INFORMATION:
; APPLICANT: Donohue, Timothy J
; APPLICANT: Barber, Robert D
; APPLICANT: Wittuhn, Vernon
; TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,182
; FILING DATE: 08/08/922,182
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/608,241
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296,93511

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
; LENGTH: 2408 base pairs
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Rhodobacter sphaeroides 2.4.1
; FEATURE:
; NAME/KEY: -35_promoter
; LOCATION: 262..267
; FEATURE:
; NAME/KEY: -10_promoter
; LOCATION: 285..290
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; NAME/KEY: CDS
; LOCATION: 346..1476
; OTHER INFORMATION: /product= "AdhI Class III Alcohol Other Information: Dehydrogenase Gene"
US-08-608-241-1

Query Match 9.5%; Score 31; DB 1; Length 2408;
Best Local Similarity 53.8%; Pred. No. 1.1; Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 27 CGCGAGGCCACACAGGGGGGAGAAGGCGCTTGAAGTGAAAGTGATGC 86
Db 351 CACCCGTCGCGCGCTGGAGCGCCAGCGCTGAGTCATGGAGGTAATC 410
QY 87 AGTAGCCCTCTGGCCCTGGATATTGTTGTTGATAACTGTGCCATCTGAGAACACA 145
Db 411 CGAGGCCAACGGGGGGAGGTCTGGTCAGATCAAGGCCACCGCACACTGCCACA 469

Query Match 9.5%; Score 31; DB 3; Length 2408;
 Best Local Similarity 53.8%; Pred. No. 1.; Mismatches 0;
 Matches 64; Conservative 0; Indels 0; Gaps 0;

Qy 27 CCCGAGCCGACACAGGGGGAGAGCGCTTGAAGTAAAAAGTGAATGC 86
 Db 351 CACCGTGCGCGCTGGCTCGGATATGTGTTGATACTCAGCAGGACACA 410
 Qy 87 AGTAGCCCTCTGGCTCGGATATGTGTTGATACTCAGCAGGACACA 145
 Db 411 CGAAGGCCCAAGGCCGCCGAGGTAGTCGAGATCAGGCCAACCGGCATGCCACCA 469

RESULT 7
 US-09-599-360B-27
 Sequence 27, Application US/09599360B
 Patent No. 654633
 GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, J. B.
 APPLICANT: Jobert, S.
 APPLICANT: Bougueret, L.
 TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
 CURRENT APPLICATION NUMBER: US/09/599, 360B
 CURRENT FILING DATE: 2000-06-21
 PRIOR APPLICATION NUMBER: 60/113, 686
 PRIOR FILING DATE: 1998-12-22
 PRIOR APPLICATION NUMBER: 60/141, 032
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: 08/469, 099
 PRIOR FILING DATE: 1999-12-21
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: Patent.Pm
 SEQ ID NO 27
 LENGTH: 648
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: CDS
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 NAME/KEY: polyA_signal
 LOCATION: 612..617
 NAME/KEY: polyA_site
 LOCATION: 62..648
 ;US-09-599-360B-27

Query Match 9.2%; Score 30; DB 4; Length 648;
 Best Local Similarity 57.4%; Pred. No. 1.; Mismatches 0; Indels 0; Gaps 0;
 Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 79 TGGAAATCGAGTGGCCCTCTGGCCCTGGGATATGTGTTGATACTCGCATCTGCAGG 138
 Db 208 TGGAAACGGCGTGGCCACTTGGCTCTGGCTGGCCAACGATGAGAAGCTGGCATCTGCAGG 267
 Qy 139 AACACATATTGGATCTTGGATAGATGTCAG 172
 Db 268 ATGGCAATTAAACGGATGCTGSCCTGACTGGCAAGG 301

RESULT 8
 US-08-386-727-7/c
 Sequence 7, Application US/08386727
 Patent No. 5792647
 GENERAL INFORMATION:
 APPLICANT: ROSEMAN, SAUL
 APPLICANT: BASSLER, BONNIE
 APPLICANT: KEYHANI, NEMAT O.
 APPLICANT: CHITLARU, EDITH
 APPLICANT: ROME, CHRIS
 APPLICANT: YU, CHARLES
 TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & RICHARDSON P. C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/600, 452A
 FILING DATE: 13-FEB-1996

Query Match 8.9%; Score 29.2; DB 1; Length 2951;
 Best Local Similarity 62.2%; Pred. No. 5.; Mismatches 28; Indels 0; Gaps 0;
 Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 3 GCGGGCGAGGATGGGGTACCCGAGGGCACCAAAGGCCGGGGCAAGAGCG 62
 Db 151 GCGGGCGAGGCGGGAGGTAAGACAGAGGCCGACAGCAATGCCAGGGAATG 92
 Qy 63 CTGGAACTGAAA 76
 Db 91 TTTTGGACTGAACA 78

RESULT 9
 US-08-60-452A-7/c
 Sequence 7, Application US/08600452A
 Patent No. 5985644
 GENERAL INFORMATION:
 APPLICANT: ROSEMAN, SAUL
 APPLICANT: BASSLER, BONNIE
 APPLICANT: KEYHANI, NEMAT O.
 APPLICANT: CHITLARU, EDITH
 APPLICANT: ROME, CHRIS
 APPLICANT: YU, CHARLES
 TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & RICHARDSON P. C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/600, 452A
 FILING DATE: 13-FEB-1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07662/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2951
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
; US-08-600-452A-7
; US-09-252-991A-9470
; ORGANISM: Pseudomonas aeruginosa
; TYPE: DNA
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US-09-7252,991A
; CURRENT FILING DATE: 1990-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-02-18
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4236
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4236
; US-09-252-991A-4236/C
; Sequence 4236, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
APPLICANT: MARC J. RUBENFIELD ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US-09-7252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4236
LENGTH: 648
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa

RESULT 10
US-09-252-991A-4236/C
; Sequence 4236, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
APPLICANT: MARC J. RUBENFIELD ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US-09-7252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4236
LENGTH: 648
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa

Query Match 8.9%; Score 29 2; DB 2; Length 2951;
Best Local Similarity 62.2%; Pred. No. 5.3; Mismatches 0; Gaps 0;
Matches 46; Conservative 0; MisMatches 28; Indels 0; Gaps 0;

QY 3 GCGCCGAGCGATGATGGATAACCCGGACGCCAACAGCGCGGGCAAGAAGCG 62
Db 151 GGCAGCGAGGGGGGGAGGTAGACAGAGCCCCGACCCAGCATGCCAGGGATG 92

QY 63 CTTTGAAAGTCGAAA 76
Db 91 TTGGTGAATGAA 78

RESULT 12
US-07-598-873-1/C
; Sequence 1, Application US/07598873
; Patent No. 5254100
; GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: GRIGERSON, DONALD
APPLICANT: RAY, JOHN A
APPLICANT: SCHUCH, WOLFGANG W
TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
TITLE OF INVENTION: DERIVED THEREFROM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/598,873
FILING DATE: 1990-01-09
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-322-0300
TELEFAX: 202-322-0304
TELEFAX: 6714622 CUSH
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1080 base Pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO
 ORIGINAL SOURCE: Lycopersicon esculentum
 ORGANISM: Lycopersicon esculentum
 STRAIN: Ailsa Craig
 DEVELOPMENTAL STAGE: Ripening

US-07-598-873-1

Query Match 8.7%; Score 28.6; DB 1; Length 1080;
 Best Local Similarity 61.3%; Pred. No. 5.2; Mismatches 29; Indels 0; Gaps 0;
 Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 221 TCTGTAAACATGCTTCACTCCACTGCATCCTCGGCTCAAACAGCACGGT 280
 Db 742 TCTTTAATTCTTGATCAATCACAATGCACTGGATTGACATAAACCT 683

Qy 281 GTCATGGACACA 295
 Db 682 GCTTGTGATACACA 668

RESULT 13

US-08-073-425-1/c

Sequence 1, Application US/08073425

Patent No. 559829

GENERAL INFORMATION:

APPLICANT: BIRD, COLIN R

APPLICANT: BONIWELL, JEREMY M.

APPLICANT: GRIERSON, DONALD

APPLICANT: RAY, JOHN A

APPLICANT: SCHUCH, WOLFGANG W

TITLE OF INVENTION: PLANTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

STREET: 1100 New York Avenue, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/073,425

FILING DATE: 09-JUN-1993

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: DEAVER, DONALD B.

REGISTRATION NUMBER: 23,048

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-822-3000

TELEFAX: 202-822-0944

TELEX: 6714627 CUSH

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1080 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Lycopersicon esculentum

STRAIN: Ailsa Craig

DEVELOPMENTAL STAGE: Ripening

US-08-396-531-1

Qy 221 TCTGTAAACATGCTTCACTCCACTGCATCCTCGGCTCAAACAGCACGGT 280
 Db 742 TCTTTAATTCTTGATCAATCACAATGCACTGGATTGACATAAACCT 683

Qy 281 GTCATGGACACA 295
 Db 682 GCTTGTGATACACA 668

RESULT 14

US-08-396-531-1/c

Sequence 1, Application US/08396531

Patent No. 5744364

GENERAL INFORMATION:

APPLICANT: BIRD, COLIN R

APPLICANT: GRIERSON, DONALD

APPLICANT: RAY, JOHN A

APPLICANT: SCHUCH, WOLFGANG W

TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS

TITLE OF INVENTION: DERIVED THEREFROM

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

STREET: Ninth Floor, 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/396,531

FILING DATE:

CLASSIFICATION: 800

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/847,037

FILING DATE: 16-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1080 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Lycopersicon esculentum

STRAIN: Ailsa Craig

DEVELOPMENTAL STAGE: Ripening

US-08-396-531-1

Qy 221 TCTGTAAACATGCTTCACTCCACTGCATCCTCGGCTCAAACAGCACGGT 280
 Db 742 TCTTTAATTCTTGATCAATCACAATGCACTGGATTGACATAAACCT 683

Qy 281 GTCATGGACACA 295
 Db 682 GCTTGTGATACACA 668

RESULT 15

US-08-073-425-1

Sequence 1, Application US/08073425

Patent No. 559829

GENERAL INFORMATION:

APPLICANT: BIRD, COLIN R

APPLICANT: GRIERSON, DONALD

APPLICANT: RAY, JOHN A

APPLICANT: SCHUCH, WOLFGANG W

TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS

TITLE OF INVENTION: DERIVED THEREFROM

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

STREET: Ninth Floor, 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/396,531

FILING DATE:

CLASSIFICATION: 800

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/847,037

FILING DATE: 16-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1080 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Lycopersicon esculentum

STRAIN: Ailsa Craig

DEVELOPMENTAL STAGE: Ripening

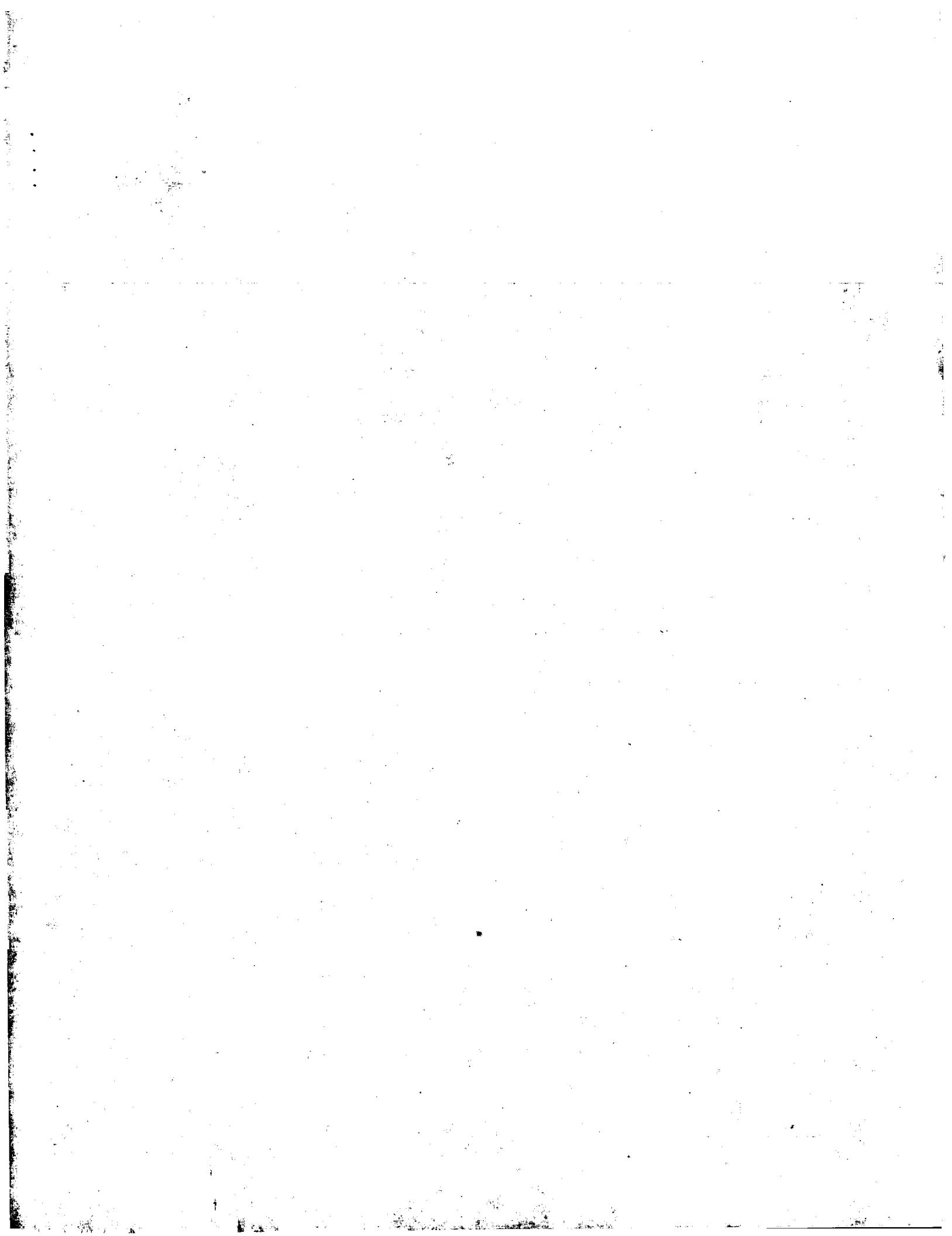
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Query Match 8.7%; Score 28.6; DB 1; Length 1080;

Best Local Similarity 61.3%; Pred. No. 5.2; Mismatches 29; Indels 0; Gaps 0;

Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 221 TCTGTAAACATGCTTCACTCCACTGCATCCTCGGCTCAAACAGCACGGT 280
 Db 742 TCTTTAATTCTTGATCAATCACAATGCACTGGATTGACATAAACCT 683Qy 281 GTCATGGACACA 295
 Db 682 GCTTGTGATACACA 668



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Om nucleic - nucleic search, using sw model

Run on: August 27, 2003, 02:48:18 ; Search time 161 Seconds

(without alignments) 4566.146 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1atggcgccagcgatggatgt.....tccaaaaggatggcactag 327

Scoring table: IDENTITY NUC

Gapov 10.0 , Gapext 1.0

Searched: 1517243 seqs, 112408182 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT1_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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Pred NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	325	99.4	476	11 US-09-918-995-17191	Sequence 17191, A
c 2	321.8	98.4	4543	14 US-10-198-846-11311	Sequence 11311, A
c 3	92.5	380	10	US-09-960-352-4677,	Sequence 4677, AP
c 4	296.8	90.8	5111	14 US-10-205-823-392	Sequence 382, AP
c 5	253.6	77.6	3208	14 US-10-214-811-27	Sequence 27, APPL
c 6	253.6	77.6	3208	14 US-10-214-811-27	Sequence 27, APPL
c 7	205.8	62.9	439	11 US-09-918-995-14771	Sequence 14771, A
c 8	183.8	56.2	175561	14 US-10-017-721-3	Sequence 20, APPL
c 9	173	52.9	390	9 US-09-707-721-20	Sequence 220, APPL
c 10	157.4	48.1	418	9 US-09-962-43-220	Sequence 2493, APPL
c 11	138.8	42.4	415	14 US-10-198-846-2493	Sequence 735, APPL
c 12	76.4	23.2	271	9 US-09-294-03B-735	Sequence 39, APPL
c 13	76	23.2	836	10 US-09-764-864-39	Sequence 498, APPL
c 14	76	23.2	836	10 US-09-764-864-498	Sequence 7, APPL
c 15	74	22.6	342	9 US-09-826-312-7	Sequence 7, APPL
c 16	22.6	342	14	US-10-108-767-7	Sequence 7, APPL

RESULT 1
US-09-18-995-17191
Sequence 17191, Application US/09918995
Publication No. US030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TIME OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09-18-995

CURRENT FILING DATE: 2001-07-30

PRIORITY APPLICATION NUMBER: US/09/235,076

PRIORITY FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 17191

LENGTH: 476

TYPE: DNA

ORGANISM: Homo sapiens

FORMAT:

NAME/KEY: misc_feature

LOCATION: ((1)..(476))

OTHER INFORMATION: n = A,T,C or G

US-09-18-995-17191

ALIGNMENTS

Query/ Match Best Local Similarity 99.4%; Score 325; DB 11; length 476; Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGCGAGCGATGAGTGGATACCCGAGGGCACACAGGGGGGGCAAGAGCG 62

Db 74 GCGGCCGCGATGGAGTGGATACCCGAGGGCACACAGGGGGCGGCACAGGG 133

Db 74 CTGTGCAATCTGCAGGACCAATTATGATCTTGATGATATGTCAGGAC 182

Db 134 CTGTGAACTGAAAGTGAATGAGTGGCTCTGGCCCTGGCTTGGTTGATAA 193

QY 123 CTGTGCAATCTGCAGGACCAATTATGATCTTGATGATATGTCAGGAC 182

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RESULT 2
US-10-198-846-11311/C
; Sequence 11311, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Tao, Neobing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEAR ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006.37-21(10288)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO: 4677
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB34-034-Q1-E1-E7
; US-09-960-352-4677

Query Match 92.5%; Score 302.4; DB 10; Length 380;
Best Local Similarity 96.6%; Pred. No. 8.9e-98;
Matches 309; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Query 8 CAGCGGATGGATGGATAACCCGAGCGGCCACACAGCGCGCGGGCAAGAAGCGCTTG 67
Db 2 CAGCGGATGGATGGATAACCCGAGCGGCCACACAGCGCGCGGGCAAGAAGCGCTTG 61
Query 68 AAGTGTAAAGATGGATTCGATGCGTASCCGCCTCGGGCTGGATATGGTTGATACTGNG 127
Db 62 AAGTGAAGAAGTGGATTCGATGCGTASCCGCCTCGGGCTGGATATGGTTGATACTGNG 121
; PRIORITY NUMBER: US/10/198,846
; PRIORITY APPLICATION NUMBER: 60/206,220
; PRIORITY FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO: 11311
; LENGTH: 4543
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-198-846-11311

Query Match 98.4%; Score 321.8; DB 14; Length 4543;
Best Local Similarity 99.4%; Pred. No. 3.2e-104; Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Query 3 GGGCGGAGCGGTGGATGTTGGAATCCCGAACAGCGGGCGGGCAAGAAGCG 62
Db 1089 GCCCCGAGCCATGGATGTTGGAATACCCGAGCGGCCACACAGCGGGCGGGCAAGAAGCG 1030

Query Match 92.5%; Score 302.4; DB 10; Length 380;
Best Local Similarity 96.6%; Pred. No. 8.9e-98;
Matches 309; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Query 188 CTACTCAGAGAGTGTACTGTCGATGGGGAGTGTGTACCATGCTTTCACTCCACT 247
Db 182 CTACTCAGAGAGTGTACTGTCGATGGGGAGTGTGTACCATGCTTTCACTCCACT 241
Query 248 GCATCTCTGGCTGGCTCAAACACACAGCAGCTGTCAGCCAAACAGCGGGAT 307
Db 122 CCATCTCGAGAACCCATATTGGATCTTGTGATAGTGTCAAGCCAAACAGCGTCGG 181
Query 308 TCCAAGAAGTAGGGACTAG 327
Db 302 GCATCTCTGGCTGGCTCAAACACACAGCAGCTGTCAGCCAAACAGCGGGAT 301
TCCAAGAAGTAGGGACTAG 321

RESULT 4
US-10-205-823-382/C
; Sequence 382, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endge, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Anderson, Dustin
; APPLICANT: Anderson, Xumei
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF PROSTATE CANCER
; FILE REFERENCE: MRT-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR APPLICATION NUMBER: 60/314,356
; RESULT 3
; Sequence 457, Application US/09960352
; Patent No. US20030107361

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PRIOR APPLICATION NUMBER: 60/325, 020
; PRIORITY FILING DATE: 2001-09-25
; PRIORITY APPLICATION NUMBER: 60/341, 746
; PRIORITY APPLICATION NUMBER: 60/362, 158
; PRIORITY FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 382
; LENGTH: 5111
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-205-823-382

Query Match 90.8%; Score 296.8; DB 14; Length 5111;
Best Local Similarity 99.3%; Pred. No. 3e-95; Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCGCAGCCTGGATACCCGACGGCACCAACAGGGCGGGCAAGAACGG 62
Db 300 GCCCCAGCGATGGATACCCGACGGCACCAACAGCGCGCAGAAGCG 241
QY 63 CTTGAGGTGAAAGTGGATGCAGTAGGCCCTGGGCTGGGATATGGTTGATAA 122
Db 240 CTTGAGGTGAAAGTGGATGCAGTAGGCCCTGGGCTGGGATATGGTTGATAA 181
QY 123 CTGGCCATCTGAGGACCATATTGGATCTGGATAGAATGTCAGTAACCGAGC 182
Db 180 CTGTGCCATCTGAGGACCATATTGGATCTGAGTAAGTGCATAGCTAACCGGC 121
QY 183 GTCCGCTACTTCAGAGAGTGACTGTGATGGAGCTGTGTAACCTGCTTCACT 242
Db 120 GTCCGCTACTTCAGAGAGTGACTGTGATGGAGCTGTGTAACCTGCTTCACT 61
QY 243 CCACGCCATCTCCTGGTCAAACAGACAGGTTGTCATGGACACAGAGAGTG 302
Db 60 CCACTGACATCTCGCTGGTCAAACACGACAGAGAGTG 1

RESULT 5
US-09-780-016-27
; Sequence 27, Application us/09780016
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; TITLE OF INVENTION: No. US20030023062A1 Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LA-0132-USA
; CURRENT APPLICATION NUMBER: US10/7214, 811
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US09/780, 016
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-214-811-27

Query Match 99.5%; Score 253.6; DB 14; Length 3208;
Best Local Similarity 98.5%; Pred. No. 7.1e-80; Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 68 AACGGAAGTGGATCCAGTAGCCCTGGGATTTGGTTGATACTGTG 127
Db 2765 AAAAAAATAATGGATCTGGATCTGGATTAACCGGCTCCG 2824
QY 128 CCATCTGGAGAACACATATGGATCTGGATAGATGTCAGCTAACCGGCTCCG 187
Db 2825 CCATCTGGAGAACACATATGGATCTGGATAGATGTCAGCTAACCGGCTCCG 2884
QY 188 CTACTCAGAAGGGTTGACTGTGCGATGGGAGTCTGTAACCATGCTTTCACCTCCT 247
Db 2885 CCATCTGGAGAACACATATGGATCTGGATAGATGTCAGCTAACCGGCTCCG 2944
QY 248 GCATCTGGAGAACACAGACAGGGTTGACATGGACAGAGAGTGGAA 307
Db 2945 GCATCTGGAGAACACAGACAGGGTTGACATGGACAGAGTGGAA 3004
QY 308 TCCAAAGTATGGCACTAG 327
Db 3005 TCCAAAGTATGGCACTAG 3024

RESULT 7

Query Match 77.6%; Score 253.6; DB 9; length 3208;
Best Local Similarity 98.5%; Pred. No. 7.1e-80; Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 68 AACGGAAGTGGATCCAGTAGCCCTGGGATTTGGTTGATACTGTG 127
Db 2765 AAAAAAATAATGGATCTGGATCTGGATTAACCGGCTCCG 2824

US-09-918-995-14771
; Sequence 14771, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 14771
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-918-995-14771

Query Match 62.9%; Score 205.8; DB 11; Length 439;
Best Local Similarity 99.0%; Pred. No. 3.6e-63; 0; Mismatches 2; Indels 0; Gaps 0;
Matches 207; Conservative

QY 78 GTGGAAATGCACTGAGTATGTTGATAACTGTGCCATCTGCAG 137
Db 231 GTGGAATGCACTTCGGCTCGGCCCTGGGAGATGTGGAG 290
Qy 138 GACCATTAATGGATCTTGATAGAATGTCAGAAGCTAACAGGCTCCGACTTCAGA 197
Db 291 GACCATTAATGGACTTTCATGAACTGCAAGGGCTCGCAG 350
Qy 198 AGAGTGTACTGPGCAGGGAGTCGTAACTGTGCCATCTGCAG 257
Db 351 AGAGTGTACTGPGCAGGGAGTCGTAACTTCACCTCACATCTCG 410
Qy 258 CTGGCTCAAAACACGAGGGTGTCCAT 286
Db 411 CTGGCTCAAAACACGAGGGTGTCCAT 439

QY 61 CGCTTTGAAGTGAARAAGTGGAAATGCACTGAGTATGTTGAGTCTGGCCCTGGGATATTGTTGTT 116
Db 59505 TGCTTGAAGTAANAAAATGAACTCCAGTAGCTAGCCCTGGCTTGGGATTTGTTGTT 59564
Qy 117 TGATTAATCTGGCCATCTGGAGGAACACATATTGATCTTGATAGAATGTCAGCTAA 176
Db 59565 TAATACTGTCGCACTCTGGAGAACATACAGCATGGTC-TGATGAAATGTCAGCTAA 59622
Qy 177 CCAGCGTCGCTACTTCAGAAGAGTGTACTGTGCCATGGGACTCTGTAACCATGCTT 236
Db 59623 CCAAGAGTCGCACTTCAGAAGTGTACCGTGCACGGGACCTGTACCGTGCCT 59682
Qy 237 TCACTCCACTGCACTCTCGCTGCTCAAACACGACAGGTGTCCTGGACACAG 296
Db 59683 TCACT-CACTGTCTCTCACTGGCCTAACACAGTGTCCCTGGACACAG 59741
Qy 297 AGAGTGGAAATTCCAAGATGGGCACTAG 327
Db 59742 ACAATTAGGAATTCCCAAAGATGGACACAG 59772

RESULT 8
US-10-017-721-3
; Sequence 3, Application US/10017721
; Publication No. US20030096248A1
; GENERAL INFORMATION:
; APPLICANT: McCarty, Jeanette
; APPLICANT: Daley, George
; APPLICANT: Bolk, Stacey
; APPLICANT: Boik, Stacey
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: WO-03-031214
; CURRENT APPLICATION NUMBER: US/10/017,721
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,033
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/330,248
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 175561
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-017-721-3

Query Match 56.2%; Score 183.8; DB 14; Length 175561;
Best Local Similarity 81.3%; Pred. No. 4.5e-51; 0; Mismatches 269; Conservative 0; Indels 20; Gaps 4;
Matches 209; Conservative

QY 1 ATGGCGGGAGGATGGATGTTGATACCCCGAGGGCACACAGGGGGGGCAAGAG 60
Db 59458 ATGGCAGGGCATGGATGGATACCCCAAGATKCCAGC---AG 59504
Qy 178 CAGGGTCCGCTACTTCAGAAGAGTGTACTTCGCAAGGAGTGTCAACATCTTT 237

QY 61 CGCTTTGAAGTGAARAAGTGGAAATGCACTGAGTATGTTGAGTCTGGCCCTGGGATATTGTTGTT 116
Db 59505 TGCTTGAAGTAANAAAATGAACTCCAGTAGCTAGCCCTGGCTTGGGATTTGTTGTT 59564
Qy 117 TGATTAATCTGGCCATCTGGAGGAACACATATTGATCTTGATAGAATGTCAGCTAA 176
Db 59565 TAATACTGTCGCACTCTGGAGAACATACAGCATGGTC-TGATGAAATGTCAGCTAA 59622
Qy 177 CCAGCGTCGCTACTTCAGAAGAGTGTACTGTGCCATGGGACTCTGTAACCATGCTT 236
Db 59623 CCAAGAGTCGCACTTCAGAAGTGTACCGTGCACGGGACCTGTACCGTGCCT 59682
Qy 237 TCACTCCACTGCACTCTCGCTGCTCAAACACGACAGGTGTCCTGGACACAG 296
Db 59683 TCACT-CACTGTCTCTCACTGGCCTAACACAGTGTCCCTGGACACAG 59741
Qy 297 AGAGTGGAAATTCCAAGATGGGCACTAG 327
Db 59742 ACAATTAGGAATTCCCAAAGATGGACACAG 59772

RESULT 9
US-09-770-791-20
; Sequence 20, Application US/09770791

Patent No. US20030062014A1

GENERAL INFORMATION:

APPLICANT: Gorlich, Jorn

APPLICANT: An, Yong-Qiang

APPLICANT: Hamilton, Carol M.

APPLICANT: Price, Jennifer L.

APPLICANT: Raines, Tracy M.

APPLICANT: Yu, Yang

APPLICANT: Rameka, Joshua G.

APPLICANT: Page, Amy

APPLICANT: Matthew, Abraham V.

APPLICANT: Ledford, Brooke L.

APPLICANT: Woessner, Jeffrey P.

APPLICANT: Haas, William David

APPLICANT: Garcia, Carlos A.

APPLICANT: Krieger, Maja

APPLICANT: Slader, Ted

APPLICANT: Davis, Keith R.

APPLICANT: Allen, Keith

APPLICANT: Hoffman, Neil

APPLICANT: Huihan, Patrick

TITLE OF INVENTION: Expressed Sequences of Arabidopsis

FILE REFERENCE: 2029 (PAR-018PV)

CURRENT APPLICATION NUMBER: US/09/770,791

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/178,480

PRIOR FILING DATE: 2000-01-27

NUMBER OF SEQ ID NOS: 999

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 20

LENGTH: 390

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-770-791-20

Query Match 52.9%; Score 173; DB 9; Length 390;

Best Local Similarity 77.7%; Pred. No. 1.9e-51; 0; Mismatches 60; Indels 0; Gaps 0;

Matches 209; Conservative

QY 58 AAGGCCTTGAAAGTGAAGAACAGTGGATGCACTGGCCCTGGGATATTGTTGTT 117
Db 110 AAGGATTCGAAATGAGAATGGCTGGCCCTGGCTCTGGGCTGGGATATCGCTT 169
Qy 118 GATACTGTGGCTTCAGGAACTTCAGGATGGCTGGCTGGCTGGGATATCGCTT 177
Db 170 GACAATGTCGCACTGGCTGGCTGGCTGGCTGGGATATCGCTT 229
Qy 178 CAGGGTCCGCTACTTCAGAAGAGTGTACTTCGCAAGGAGTGTCAACATCTTT 237

RESULT 10
US-09-962-436-220/c
; Sequence 220, Application US/09962436
; Patent No. US20020051301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 688290-75
; CURRENT APPLICATION NUMBER: US/09/962 436
; CURRENT FILING DATE: 2001-09-25
; PRIORITY NUMBER: US/60/235, 082
; PRIORITY FILING DATE: 2000-09-25
; PRIORITY FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 220
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-962-436-220

Query Match
Best Local Similarity 85.4%; Score 157.4; DB 9; Length 418;
Matches 199; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

Qy 95 TCGGGCTGGATATTGTTGTTGATACTCTGGCCATCTGAGAACCATTTATGGTC 154
Db 417 TCGGGCTGGATATTGTTGTTGATACTCTGGCCATCTGAGAACCATTTATGGTC 358

Qy 155 TTGCACTGAATCAGCTAACAGGCCACTTGTGAGAGTGACTGTCGCACT 214
Db 357 -TGCATHTGAATGTCAACTAACCAAGTGTGCGTCAAGTGTACGGTGAC 300

Qy 215 GGGAGTGTGTAACATGCTTGTACTTCAGAGAGTGACTGTCATCTGGCTCAAAACAGAC 274
Db 299 GGGGAGCTGTAACTGGTCAACGGCTTTCACT-CACTGTCTCTGACTGGCTCAACACAGAC 241

Qy 275 AGGTGTCTGACAGACAGAGAGTGGAATTCACAAAGATGGCTCAACACAGAC 327
Db 240 AGGTGTCTGACAGACAGACAGACATGGAAATCCAAAGTGTGACACAGAC 188

RESULT 11
US-10-198-046-2493
; Sequence 2493, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198, 846
; CURRENT FILING DATE: 2002-07-18
; PRIORITY NUMBER: US/03/06, 220
; PRIORITY FILING DATE: 2001-07-18

Query Match
Best Local Similarity 70.6%; Score 76.4; DB 9; Length 271;
Matches 115; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

Qy 19 GTGGATAACCCGAGGGACCAACAGCGCCGGCAAGAAGGCGCTTGAAGTGAAAG 78
Db 110 GTCGGTGGTCCGGCTCTCTCATCTCCCGAACGCCAACAGGCTTGAGATCAAAG 169

Qy 79 TGGATGGATGACCCCTGGGCTGGGATATGGTGTGATACTGGCCATCTGGAGG 138
Db 170 TGGACCGCGCTGGCTCTGGGATATGGTGTGAGCA-TGCGCNATCTGCCG 228

Qy 139 AACACATATGCTACTGCTAGAATGTCAGAATGCAACGTAACAG 181
Db 229 AACACATATGCTACTGCTAGAATGCAACGTAACAG 271

RESULT 12
US-09-294-093B-735
; Sequence 735, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Ito, laura, Y.
; APPLICANT: Laligudi, Raghunath, V.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294, 093B
; CURRENT FILING DATE: 1999-04-16
; PRIORITY NUMBER: 60/082, 567
; PRIORITY FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 735
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte
; NAME/KEY: unsure
; LOCATION: 89, 219
; OTHER INFORMATION: a, t, c, g, or other
; US-09-294-093B-735

Query Match
Best Local Similarity 70.6%; Score 76.4; DB 9; Length 271;
Matches 115; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

Qy 19 GTGGATAACCCGAGGGACCAACAGCGCCGGCAAGAAGGCGCTTGAAGTGAAAG 78
Db 110 GTCGGTGGTCCGGCTCTCTCATCTCCCGAACGCCAACAGGCTTGAGATCAAAG 169

Qy 79 TGGATGGATGACCCCTGGGCTGGGATATGGTGTGATACTGGCCATCTGGAGG 138
Db 170 TGGACCGCGCTGGCTCTGGGATATGGTGTGAGCA-TGCGCNATCTGCCG 228

Qy 139 AACACATATGCTACTGCTAGAATGTCAGAATGCAACGTAACAG 181
Db 229 AACACATATGCTACTGCTAGAATGCAACGTAACAG 271

NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2493
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5
; OTHER INFORMATION: n = A,T,C or G
; US-10-198-846-2493

Query Match
Best Local Similarity 98.6%; Score 138.8; DB 14; Length 415;
Matches 140; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Patents 1 ATGGGGAGCGGAGGATGGGATGGGATGGGACCCGGGACCAACGGGCGGGCGGAGAG 60
; Db 91 ATGGGGAGCGGAGGATGGGATGGGATGGGACCCGGGACCAACGGGCGGGAGAG 150
; Qy 61 CGCTTGAGTGAAGAACGGTGGAGTGGCTCTGGCCCTGGGATATTGGTGTAT 120
; Db 151 CGCTTGAGTGAAGAACGGTGGAGTGGCTCTGGCCCTGGGATATTGGTGTAT 210

Qy 121 AACTGTGCCATCTGGAGAAC 142
Db 211 AACTGTGCCATCTGGAGAAC 232

RESULT 13
US-09-764-864-39
; Sequence 39, Application US/09764864
; Patent No. US2002132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-864-39

Query Match 23.2%; Score 76; DB 10; Length 836;
Best Local Similarity 56.9%; Pred. No. 1.4e-16; Matches 164; Conservative 0; Mismatches 115; Indels 9; Gaps 1; Qy 26 CCCCCGAGCGACCAACACAGGGCCGGGAAAGAACGCGCTTGAATGAAAAGTGGAATG 85
Db 65 CCGGGAGCTCAGGGTCCAAAGTCGGGAGGACAGATGTTCTCCCTCAAAGAGTGAC 124
Qy 86 CACTAGGCCTCTGGCTCTGGATATTGTGGTGTGAACTGTCATCTGCCAGGAAACCA 145
Db 125 CGGGGCCATGTGGACGTGGAGCTGGGCAATCGTGCAGGTCCAG 184
Qy 146 TTATGATCTTGCATAAGATGTCAGCTAACAGGGCTCGCTACTTGAGAAGGTGA 205
Db 185 TGATGGATGTCGCTGTTAGATGTCAAAGCTGAA - - - - - CAAACAGAGGACTG 235
Qy 206 CTGTCGATGGGGAGCTGAACCTGCCTACTGATCTCTGCGCTCA 265
Db 236 TTGGCTCTGGGAGAACTATCTCTCCACACTGCTGCAATGTCCTGTGGGTA 295
Qy 266 AACAGACGACAGGGTGTCCATTGACAAAGAGAGGTGGSAATTCCAA 313
Db 296 AACAGAACATCGCTGCCCTCTGCCAGCAGGACTGGGGTCCAA 343

RESULT 14
US-09-764-864-498
; sequence 498, Application US/09764864
; Patent No. US2002132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 498
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-864-498

Query Match 22.6%; Score 74; DB 9; Length 342;
Best Local Similarity 58.4%; Pred. No. 4.9e-16; Matches 153; Conservative 0; Mismatches 100; Indels 9; Gaps 1; Qy 52 GGCAMANGGCCCTTGAAAGTGGATGGCTAGGCCCTGGGCTGGGATATT 111
Db 76 GGCAGACAAAGATGTTCTCCCTCAAAGAGTGGATGCCATGGACCTGGACGTG 135
Qy 112 GTGGTGTGATACTGTCATGAGGAAACCAATATGGTCTCTTGATAGAATGTCAA 171
Db 136 GAGTCGATAGCTGGCCATCTGCAGGTCCAGGTGATGATGCGCTGTCTAGTCAA 195
Qy 172 GCTAAACGAGGGCTCGCTACTCAGAAGACTGACTGTCGCAATGGGAACTCAT 231
Db 196 GCTGAAA - - - - - CAACAAAGAGGACTGTTGTGTTGGGAGATGTATCAT 246
Qy 232 GCTTTCACCTCCACTGCACTCTGCTGCCAACACGACAGGTGCTCCATTGGAC 291
Db 247 TCCTTCACACACTGTCATGTCATGTCCTGCTGGGTGAACAGAACAACTGCTGCCCTCTGC 306
Qy 292 AACAGAGAGGGAAATTCCA 313
Db 307 CAGCAGGACTGGGTGTCAA 328

RESULT 15
US-09-826-312-7
; Sequence 7, Application US/09826312
; Patent No. US2002042083A1
; GENERAL INFORMATION:
; APPLICANT: Issakan, Starkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Piy, Todd R.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: A-68613-1-RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/826, 312
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-826-312-7

Query Match 22.6%; Score 74; DB 9; Length 342;
Best Local Similarity 58.4%; Pred. No. 4.9e-16; Matches 153; Conservative 0; Mismatches 100; Indels 9; Gaps 1; Qy 52 GGCAMANGGCCCTTGAAAGTGGATGGCTAGGCCCTGGGCTGGGATATT 111
Db 76 GGCAGACAAAGATGTTCTCCCTCAAAGAGTGGATGCCATGGACCTGGACGTG 135
Qy 112 GTGGTGTGATACTGTCATGAGGAAACCAATATGGTCTCTTGATAGAATGTCAA 171
Db 136 GAGTCGATAGCTGGCCATCTGCAGGTCCAGGTGATGATGCGCTGTCTAGTCAA 195
Qy 172 GCTAAACGAGGGCTCGCTACTCAGAAGACTGACTGTCGCAATGGGAACTCAT 231
Db 196 GCTGAAA - - - - - CAACAAAGAGGACTGTTGTGTTGGGAGATGTATCAT 246
Qy 232 GCTTTCACCTCCACTGCACTCTGCTGCCAACACGACAGGTGCTCCATTGGAC 291
Db 247 TCCTTCACACACTGTCATGTCATGTCATGTCCTGCTGGGTGAACAGAACAACTGCTGCCCTCTGC 306
Qy 292 AACAGAGAGGGAAATTCCA 313
Db 307 CAGCAGGACTGGGTGTCAA 328

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OM protein - nucleic search, using frame_plus_p2n model

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 (without alignments)
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Sequence:

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 Fgapop 6.0 , Fgapext 7.0
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-NO_MMAR -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=0.5 -DELOP=6 -DELEXT=7
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5: /cgn2_6/ptodata/2/inna/PCTVS_COMBO.seq:*
6: /cgn2_6/ptodata/2/inna/backfileseq.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	501.5	81.4	3208	Sequence 27, Appl
2	262.5	42.6	301	Sequence 492, App
3	217.5	35.2	648	Sequence 27, Appl
4	90	14.6	8438	Sequence 1, Appl
5	85	13.8	2339	Sequence 11, Appl
6	85	13.8	2505	Sequence 1, Appl
7	85	13.8	2517	Sequence 7, Appl
8	83	13.5	315	Sequence 4, Appl
9	81.5	13.2	4259	Sequence 2, Appl
10	81.5	13.2	4259	Sequence 2, Appl
11	80	13.1	804	Sequence 881, Appl
12	13.0	944	2	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-780-016-27

; Sequence 27, Application US/09780016

; Patent No. 650956

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

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QY 16 GlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrp 35 ; Patent No. 6548633
Db 2752 GGACCATAAAAAAAGA-----AAAATGGATGCAAGTCAGCTCGCCCTGG 2802 ; GENERAL INFORMATION:
QY 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspIleCysIleGlu 55 ; APPLICANT: Dumas Mine Edwards, J. B.
Db 2803 GATATTGTGGTGTGATACTGTGCCATCTGCAGAACACANTATGATCTTGATGAA 2862 ; APPLICANT: Bouquellet, L.
QY 56 CysGlnAlaLysGlnAlaSerAlaLysSerGluGluCystThrValAlaTrpGlyAlaCys 75 ; APPLICANT: Jober, S.
Db 2863 TGTCAACTAACCGGGTCCGCTACTTCACATCTGCCTGCTGCTCAAACACAGGTTGTC 2922 ; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
QY 76 AsnHistAlpheHisPheHisCysIleSerArgTrpLeuThrArgGlnValCysPro 95 ; FILE REFERENCE: GENSET.050CP3
Db 2923 AACATGCTTTCACITCCACTGCATCTGCCTGCTGCTCAAACACAGGTTGTC 2982 ; CURRENT APPLICATION NUMBER: US/09/599, 360B
QY 96 LeuAspAsnArgGluLrpGluPheGlnLysTyrglyHs 108 ; PRIORITY FILING DATE: 1999-06-25
Db 2983 TTGGACACAGAGTAGGGAAATTCAAAGTATGGCAC 3021 ; PRIORITY APPLICATION NUMBER: 60/113, 686
RESULT 2 ; PRIORITY FILING DATE: 1999-12-21
US-09-313-294A-492 ; NUMBER OF SEQ ID NOS: 123
; Sequence 492, Application US/09313294A ; SOFTWARE: Patent.pn
; GENERAL INFORMATION: ; SEQ ID NO: 27
; PATENT NO: 6476212 ; LENGTH: 648
; APPLICANT: Laigudi, Raghunath V. ; TYPE: DNA
; APPLICANT: Ito, Laura Y. ; ORGANISM: HOMO Sapiens
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR ; FEATURE:
; FILE REFERENCE: PL-0017 US ; NAME/KEY: cDS
; CURRENT APPLICATION NUMBER: US/09/313, 294A ; LOCATION: 107, 438
; NUMBER OF SEQ ID NOS: 7600 ; NAME/KEY: polyA.signal
; SOFTWARE: PERL Program ; LOCATION: 612, 617
; SEQ ID NO: 492 ; NAME/KEY: polyA_site
; LENGTH: 301 ; LOCATION: 632, 648
; TYPE: DNA ;
; ORGANISM: zeb maya
; FEATURE: ;
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. 6476212 70054933H1 ;
; US-09-313-294A-492 ;
Alignment Scores: ;
Pred. No.: 1.91e-24 ; Score: 2.79e-18 ; Length: 648 ;
Score: 262.50 ; Matches: 301 ; Matches: 43 ;
Percent Similarity: 71.43% ; Conservative: 4 ; Conservatice: 18 ;
Best Local Similarity: 65.23% ; Mismatches: 40 ;
Query Match: 42.61% ; Indels: 35.23% ; Indels: 36 ;
DB: ; Gaps: 2 ; Gaps: 3 ;
US-09-541-462B-2 (1-108) x US-09-599-360B-27 (1-648) ;
QY 2 AlaAlaAlaMetAspValAspThrProSerGlyLysAlaGlyLysLysArg 21 ;
Db 49 GCGCGACGTGGTGTITTAACCTCCGGCGGGACGCCGGCGCTGCCAACGGAGG 108 ;
QY 109 GCGGAGACGGAGTTTCGTCATGTTGCCAGGCCATTGAGATCTTGAAGATATCCTCA 168 ;
Db 22 PheGlu----- ;
QY 24 ----- ;
Db 169 ACGTGAGGCTCTGGCATGAGGTTAAGGTTAAGGCTGCGAACGGCGTGG 228 ;
QY 34 AlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspIleCys 53 ;
Db 229 CTCGGGGCCACAGTAGAGACTGGCATCTGCAGGTGGCATTAACGGATGCTGC 288 ;
QY 54 IleGluCysGlnAlaLysGlnAlaSerAlaThrSerGluGluCystThrValAlaTrpGly 73 ;
Db 289 CCTGACTGCAAG----- ;
QY 74 ValCysIleHisAlpheHisPheHisCysIleSerArgTrpLeuThrArgGlnVal 93 ;
Db 334 CAGTGGCCCACTGCTCCACATGGTCACTCCATGCTGCTGCTGCGCTATCGCCGCAAC 393 ;
QY 48 HistIleMetAspIleCysIleGluCysCysAlaLysGlnAlaSerAlaThr 64 ;
Db 250 CACATCATGATCTATGCATGAGTGGCAGGCCAACCAAGGCCAGCGCGACC 300 ;
RESULT 3 ;
US-09-599-360B-27 ;
; Sequence 27, Application US/09599360B ;
; GENERAL INFORMATION:

RESULT 4 ;
US-07-945-283-1/C ;
; Sequence 1, Application US/07945283 ;
; Patent No. 5352956 ;
; GENERAL INFORMATION:

APPLICANT: Cheung, Andrew K.
 APPLICANT: Wasley, Ronald D.
 TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
 TITLE OF INVENTION: Involving The EPO and LIL Genes
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSE: CURTIS P. Ribando
 STREET: 1815 NO. 5352596th University Street
 CITY: Peoria
 STATE: IL
 COUNTRY: USA
 ZIP: 61604

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/945, 283
 FILING DATE: 19920911
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Ribando, Curtis P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 309-685-4011 ext.513
 TELEFAX: 309-685-4128

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 8438 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:
 ORGANISM: Pseudorabies virus

FEATURE:
 NAME/KEY: CDS
 LOCATION: 622..6495

FEATURE:
 NAME/KEY: variation
 LOCATION: replace(1099, "g")

FEATURE:
 NAME/KEY: variation
 LOCATION: replace(1267, "t")

FEATURE:
 NAME/KEY: variation
 LOCATION: replace(1381, "C")

FEATURE:
 NAME/KEY: variation
 LOCATION: replace(1566, "C")

FEATURE:
 NAME/KEY: variation
 LOCATION: replace(7010, "g")

US-07-945-283-1

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	0.585	2339	24	10	22	28	4
	85.00						
	40.48%						
	28.57%						
Query Match:	3						
DB:							

US-09-541-462B-2 (1-108) x US-09-268-140-11 (1-2339)

QY 20 LysArgPheGluValLysLystrpAsnAlaValAlaLeuTrpAlaTrpAspIle----- 37

Db 1635 CGTAGGACTGCTGTGAGAAATTATTCACCT-----GAATAAAGGG 1682

QY 38 -----ValValAspAsnCysAlaLeuCysArgAsnHisIleMetAspLeu 52

Db 1683 AGCCGCTTACAGAAATAATGATGATGATGCACTGTCTATCAGAGTT----- 1733

QY 53 CysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluLucysthrValAlaTrp 72

Db 1734 -----ACACATCTCTCTCTATTACA----- 1754

QY 73 GlyValCysAsnHiaAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgIn 92

Db 1755 --CCGTGTAATCATATTTCATGCACTTGCCTTGGAATGGCTGTACATTCAAGAT 1811

QY 93 ValCysProLeu 96

Db 1812 ACTTGCCAAG 1823

RESULT 6

US-09-541-462B-2 (1-108) x US-07-945-283-1 (1-8438)

QY 6 AspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLys 25

Db 1568 GATGTRAGTGGTCCC-----GAGGGTCCCGGTTG-GCCGGGGAGTGTAGA 1522

QY 26 LystPaspAsnAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaLeuCys 45

OY

Db 1521 CGATGG-----TGGCCGTCATG----GAATGCCCTCTGC 1489

QY 46 ArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSer 65

Db 1488 -----CTGGACCGTC-----GCCCCCACC 1471

QY 66 GluGluCysthrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSer 85

Db 1470 GAGGCCAGACGCTGCG-----TGCATGCAACAGTCTGCTGACTGCATCAG 1420

QY 86 ArgTrpLeuLysThrArgGlnValCysProLeuAspAsn 98

Db 1419 CGCTGACCCCTGACGAGCACCGCCTGCCGCTGTGCAAT 1381

RESULT 5

US-09-268-140-11

; Sequence 11, Application US/09268140

; GENERAL INFORMATION:

; PATENT NO. 6268176

; APPLICANT: Gemmill, Robert M.

; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED

; FILE REFERENCE: 93445-0004

; CURRENT APPLICATION NUMBER: US/09/268, 140

; CURRENT FILING DATE: 2000-03-12

; PRIOR APPLICATION NUMBER: US 60/077, 723

; PRIOR FILING DATE: 1998-03-12

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 11

; LENGTH: 2339

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-268-140-11

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	0.585	2339	24	10	22	28	4
	85.00						
	40.48%						
	28.57%						
Query Match:	3						
DB:							

US-09-541-462B-2 (1-108) x US-09-268-140-11 (1-2339)

QY 20 LysArgPheGluValLysLystrpAsnAlaValAlaLeuTrpAlaTrpAspIle----- 37

Db 1635 CGTAGGACTGCTGTGAGAAATTATTCACCT-----GAATAAAGGG 1682

QY 38 -----ValValAspAsnCysAlaLeuCysArgAsnHisIleMetAspLeu 52

Db 1683 AGCCGCTTACAGAAATAATGATGATGCACTGTCTATCAGAGTT----- 1733

QY 53 CysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluLucysthrValAlaTrp 72

Db 1734 -----ACACATCTCTCTATTACA----- 1754

QY 73 GlyValCysAsnHiaAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgIn 92

Db 1755 --CCGTGTAATCATATTTCATGCACTTGCCTTGGAATGGCTGTACATTCAAGAT 1811

QY 93 ValCysProLeu 96

Db 1812 ACTTGCCAAG 1823

FILE REFERENCE: 93445-0004A
 CURRENT APPLICATION NUMBER: US/09/268,140
 CURRENT FILING DATE: 2000-03-12
 PRIOR APPLICATION NUMBER: US 60/077,723
 PRIOR FILING DATE: 1998-03-12
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 2505
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (238)..(2232) .
 DB: US-09-268-140-1

Alignment Scores: 0.642 Length: 2505
 Score: 85.00 Matches: 24
 Percent Similarity: 40.48% Conservative: 10
 Best Local Similarity: 40.57% Mismatches: 22
 Query Match: 13.80% Indels: 28
 Gaps: 4

US-09-541-462B-2 (1-108) x US-09-268-140-1 (1-2505)

Qy 20 LysArgpheGluValLysLystPasnAlaValAlaLeutrpAlaTrpAspIle----- 37
 Db 1813 CGTAGGACTGCTGTAGAGAAATTATTCACTrpCCT-----GAATAAAAGGG 1860

Qy 38 -----ValValAspAsnCysAlleCysArgAsnHisIleMetAspLeu 52
 Db 1849 AGCCGCTTACAAGAAATAATGTCGTAATGCAATCTGCATTCGAGTT----- 1899

Qy 53 CysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGlyCysThrValAlaTrp 72
 Db 1912 -----ACACATCCTGCTCATATACA----- 1932

Qy 93 ValCysProLeu 96
 Db 1990 ACTTGTCGAAATG 2001

RESULT 8
 US-09-325-932A-4
 ; Sequence 4, Application US/09325932A
 ; Patent No. 6451604
 ; APPLICANT: Flinn, Barry
 ; ATTORNEY: Lasham, Annette
 ; TITLE OF INVENTION: Compositions affecting programmed cell
 ; FILE REFERENCE: 1022
 ; CURRENT APPLICATION NUMBER: US/09/325,932A
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 206
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 315
 ; TYPE: DNA
 ; ORGANISM: Pinus radiata
 ; US-09-325-932A-4

Alignment Scores: 0.0674 Length: 315
 Score: 83.00 Matches: 17
 Percent Similarity: 38.18% Conservative: 4
 Best Local Similarity: 30.91% Mismatches: 20
 Query Match: 13.47% Indels: 14
 DB: 4 Gaps: 1

US-09-541-462B-2 (1-108) x US-09-325-932A-4 (1-315)

Qy 42 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61
 Db 74 TrpCGGGGTTGTCAGTCAGTCGAACTCATCCCAAGTGCAGGCAATTCACATC 151

Qy 82 HisCysIleSerArgTrpLeuLysthrArgGlnValCysProLeu 96
 Db 152 GATTGCAATCGATTATTGGCTTGAGAACCTCAAGCTGGCCCGCTC 196

RESULT 9
 US-09-816-155B-2
 ; Sequence 2, Application US/08816155B

Patent No. 5990091
 GENERAL INFORMATION:
 APPLICANT: TARTAGLIA, JAMES
 APPLICANT: COX, WILLIAM I.
 APPLICANT: GETTIG, RUSSELL R.
 APPLICANT: MARTINEZ, HECTOR
 APPLICANT: PAOLETTI, ENZO
 APPLICANT: PINCUS, STEVEN E.
 TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
 NUMBER OF INVENTIONS: METHODS OF MAKING AND USES THEREOF
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
 STREET: 745 FIFTH AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10151
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/816,155B
 FILING DATE: 12-MAR-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: KOWALSKI, THOMAS J.
 REGISTRATION NUMBER: 32,147
 REFERENCE/DOCKET NUMBER: 454310-2990
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-588-0800
 TELEFAX: 212-588-0500
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4259 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-816-155B-2

Alignment Scores:
 Pred. No.: 3.64 Length: 4259
 Score: 81.50 Matches: 22
 Percent Similarity: 36.14% Conservative: 8
 Best Local Similarity: 26.51% Mismatches: 22
 Query Match: 13.23% Indels: 31
 DB: 2 Gaps: 4

US-09-541-462B-2 (1-108) x US-08-816-155B-2 (1-4259)

QY 42 CysAlaLeuCysArgAsnHisIleMetAspLeuCysIleIleGluCysGlnAlaAsnGlnAla 61
 |||:::||| |||:::||| |||:::|||
 145 TGTGGCTTGCTAGAGAAATTAACGAAAGAACATAAACAA----- 192

QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyVal-----CysAsnHisAla 78
 ::|||:::||| |||:::|||
 DB 193 -----TATTCCGTTATTCACAAATTGTACACCG 225

QY 42 CysAlaLeuCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61
 |||:::||| |||:::|||
 79 PheHisPheHisCysIleSerArgTrpLeuLys-----ThrArgGln 92
 |||:::||| |||:::|||
 DB 226 TTTGGTTTAACTGATAAACGTTGGATGCTATAATAAAGGTACGGATCCGAAGGT 285

QY 93 ValCysPro-----LeuAspAsnArgGlutRpGluPhe 103
 |||:::|||
 DB 286 ACATGTCCTCTATGAGAACAGTTCTGTTATTATAGGCCTAAAGTAGTACTGGATAGAC 345

QY 104 GluLysTyr 106
 |||:::|||
 DB 346 GATAATAT 354

Alignment Scores:
 Pred. No.: 3.64 Length: 4259
 Score: 81.50 Matches: 22
 Percent Similarity: 36.14% Conservative: 8
 Best Local Similarity: 26.51% Mismatches: 22
 Query Match: 13.23% Indels: 31
 DB: 3 Gaps: 4

US-09-079-587-2 (1-108) x US-09-079-587-2 (1-4259)

QY 42 CysAlaLeuCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61
 |||:::||| |||:::|||
 145 TGTGGCTTGCTAGAGAAATTAACGAAAGAACATAAACAA----- 192

QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyVal-----CysAsnHisAla 78
 ::|||:::||| |||:::|||
 DB 193 -----TATTCCGTTATTCACAAATTGTACACCG 225

QY 79 PheHisPheHisCysIleSerArgTrpLeuLys-----ThrArgGln 92
 |||:::||| |||:::|||
 DB 226 TTTGGTTTAACTGATAAACGTTGGATGCTATAATAAAGGTACGGATCCGAAGGT 285

QY 93 ValCysPro-----LeuAspAsnArgGlutRpGluPhe 103
 |||:::|||
 DB 226 TTTGGTTTAACTGATAAACGTTGGATGCTATAATAAAGGTACGGATCCGAAGGT 285

QY 93 ValCysPro-----LeuAspAsnArgGlutRpGluPhe 103
 |||:::|||

Db 286 ACATGTCCTGATGAGAACAGTTCTGTATTATAGGCCATAATGGTACTGGATAGAC 345
 Qy 104 GlnLysTyr 106
 Db 346 GATAAATAT 354

RESULT 11
 US-08-998-416-881
 Sequence 881, Application US/08998416
 ; PATENT NO. 623964
 ; GENERAL INFORMATION:
 ; APPLICANT: Philippson, Peter
 ; APPLICANT: Pohlmann, Rainer
 ; APPLICANT: Steiner, Sabine
 ; APPLICANT: Mohr, Christine
 ; APPLICANT: Wendland, Jurgen
 ; APPLICANT: Knechtel, Philipp
 ; APPLICANT: Reiblchung, Corinne
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
 NUMBER OF SEQUENCES: 1152
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6239264 artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 27709
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/998.416
 FILING DATE: 24-DEC-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: CH 0016/97
 FILING DATE: 31 DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: PE-5-30306/A/C/GC1976
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8869
 TELEFAX: 919-541-8869
 INFORMATION FOR SEQ ID NO: 881:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 804 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE: ORGANISM: PAG1552RP
 US-08-998-416-881

Alignment Scores:
 Pred. No.: 0.499 Length: 804
 Score: 80.50 Mat Chas: 13
 Percent Similarity: 66.67% Conservative: 5
 Best Local Similarity: 48.15% Mismatches: 6
 Query Match: 13.07% Indels: 3
 DB: 3 Gaps: 1

US-09-541-462B-2 (1-108) x US-08-998-416-881 (1-804)
 Qy 73 GLYAlaCysAsnHisAlaPheHisPheHisCysteSerArgTrpLeuLysThr---- 90
 Db 8 GGCTCATGCCACAGAACCTCACGTCAGTGCTCACACCTCCACG 67

Qy 91 --ArgGlnValCysProLeu 95

Db 68 TCCAAGGGCCTCTGTCGATG 88
 RESULT 12
 US-08-716-605-4
 Sequence 4, Application US/08716600
 ; GENERAL INFORMATION:
 ; PATENT NO. 5861495
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Coleman, Roger
 ; APPLICANT: Goli, Surva K.
 TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/7166,606
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy RJ
 REGISTRATION NUMBER: 35,749
 REFERENCE/DOCKET NUMBER: PF-0173 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 944 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-786-606-4

Alignment Scores:
 Pred. No.: 0.718 Length: 944
 Score: 80.00 Matches: 29
 Percent Similarity: 39.81% Conservative: 12
 Best Local Similarity: 28.16% Mismatches: 18
 Query Match: 12.99% Indels: 44
 DB: 2 Gaps: 7

US-09-541-462B-2 (1-108) x US-08-786-606-4 (1-944)
 Qy 1 MetAlaAlaAlaMetAspValAsp--ThrProSerGlyLysThr-----Sergly 16
 Db 98 ATGGGAGCAGGGAGGAGGACGGGGCCGAGGGCAAAATGCGAGCGGGCGGG 157
 Qy 17 AlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAsp 36
 Db 158 GGGGC---GGGACCTTCGAA----- 175
 Qy 37 IleValValAspAsnCysAlaLeuCysArgAsnHisIleMetAspLeuCysIleGlyCys 56
 Db 176 -----TGTAAATATGTTGGAG--- 193
 Qy 57 GlnAlaAsnGlnAlaSerAlaThrSerGluGlucySthrValAlaTrpAlaCysAsn 76

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 27, 2003, 03:48:39 ; Search time 818 seconds

(without alignments) 302,908 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAMDVDTPSGTNSAGKK..... KTRQVCPLDNRNWEFQKYGH 108

Scoring table: BLOSUM62

Xgapext 10.0 , Xgapext 0.5

Ygapext 10.0 , Ygapext 0.5

Fgapext 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1533700 seqs, 1147125425 residues

Total number of hits satisfying chosen parameters: 3067400

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-MODEL=frame+P2n.model -DEV=xlh
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-TRANS=human40.cdl -LIST=5 -DOCALLIGN=200 -THR_SCORE_PCT= -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFILE=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US091164_@CGN_1_1_164_@runat_22082003-155807_25523
-NCPU=6 -ICPU=3 -NO_MAP -LARGE_SCORES=0 -WAIT_DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Published_Applications_NA:*

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4: /cgcn2_6/podata/2/pubpna/US07_NEW_PUB_seq:*
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6: /cgcn2_6/podata/2/pubpna/PCRSUS_PUBCOMB.seq:*
7: /cgcn2_6/podata/2/pubpna/US08_NEW_PUB_seq:*
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10: /cgcn2_6/podata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgcn2_6/podata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgcn2_6/podata/2/pubpna/US09_NEW_PUB_seq:*
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14: /cgcn2_6/podata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgcn2_6/podata/2/pubpna/US10_NEW_PUB_seq:*
16: /cgcn2_6/podata/2/pubpna/US60_NEW_PUBCOMB.seq:*
17: /cgcn2_6/podata/2/pubpna/us60_pubcomb.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	611	99.2	476	11 US-09-918-995-17191 Sequence 17191, A

RESULT 1
US-09-918-995-17191
Sequence 17191, Application US/09918995
Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09-918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SEQ ID LENGTH: 476

SOFTWARE: FASTSEQ for Windows Version 3.0

ORGANISM: Homo sapiens

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: (1)..(476)

OTHER INFORMATION: n = A,T,C or G

SEQ ID NO: 17191

ALIGNMENTS

Sequence 11311, A
Sequence 4677, App
Sequence 382, App
Sequence 20, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 14771, A
Sequence 3, Appl
Sequence 220, App
Sequence 39, Appl
Sequence 498, App
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 2493, App
Sequence 8547, App
Sequence 8547, App
Sequence 77, Appl
Sequence 735, App
Sequence 2188, App
Sequence 487, App
Sequence 20531, A
Sequence 38, Appl
Sequence 202, App
Sequence 1814, App
Sequence 1952, App
Sequence 365, App
Sequence 15085, A
Sequence 8855, App
Sequence 21338, A
Sequence 12407, A
Sequence 162982, Sequence 162983
Sequence 803, App
Sequence 12264, A
Sequence 629, App
Sequence 593, App
Sequence 1260, App

Alignment Scores:
 Pred. No.: 1.02e-74 Length: 476
 Score: 611.00 Matches: 107
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 99.19% Indels: 0
 DB: 11 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-918-995-17191 (1-476)

QY 2 AlaAlaAlaMetAspValAspLysPheThrProSerGlyAlaGlyLysLysArg 21
 Db 75 GCGGCAGCAGATGGATGGATACCCGAGCGCACACAGGGCGGGCAGAAGCC 134
 QY 22 PheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAspAsn 41
 Db 135 TTGAGTGAAGAAAGTGGAGATTCAGTAGCCCTGGCATGGATATTGTGGTTGATAAC 194
 QY 42 CysAlaLeuCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61
 Db 195 TGTGCCATCTGCAGGAACCACATTATGATCTTGATAGATGTCAGCTAACAGCCG 254
 QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe 81
 Db 255 TCCGCTACTCTGAGAAGCTGACTGCCCAGGGACTCTGAAACAGCTTCACITC 314
 QY 82 HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgLysPhe 101
 Db 315 CACTGATCTCAGCTGCTGCTCAAACACAGACAGGTGTCATTGGACAAAGAGCTGG 374
 QY 102 GluPheGlnLysTyrGlyHis 108
 Db 375 GAATTCAAAAGTATGGCAC 395

RESULT 2
 US-10-198-846-11311/C
 ; Sequence 11311, Application US/10198846
 ; Publication No. US0030099994A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lille, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youchen
 ; APPLICANT: Steimann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TREATMENT OF BREAST CANCER
 ; FILE REFERENCE: MRI-049
 ; CURRENT APPLICATION NUMBER: US/10/198,846
 ; CURRENT FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/306,220
 ; NUMBER OF SEQ ID NOS: 14084
 ; SEQ ID NO: 11311
 ; LENGTH: 4543
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: Clone ID: 20-LIB34-034-Q1-E1-E7
 ; SEQ ID NO: 4677
 ; LENGTH: 380
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 20-LIB34-034-Q1-E1-E7
 ; SEQ ID NO: 4677
 ; LENGTH: 380
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-198-846-11311

Alignment Scores:
 Pred. No.: 8.61e-73 Length: 380
 Score: 595.00 Matches: 103
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 98.10% Mismatches: 0
 Query Match: 96.75% Indels: 0
 DB: 10 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-960-352-4677 (1-380)

QY 4 ALAMETAPVALASPLASPTHRPROSERGLYALAGLYLYSLYSARGPHEGLU 23
 Db 64 GTGAGTGGATGGATACCCGAGCGCACACAGGGCGGGCAAGACGCCCTTCAA 63
 QY 24 VALYLSTPLRASNVALAVALALEUTPAPATRASPILERVALASPNSCYSALA 43
 Db 64 GTGAGTGGATGGATACCCGAGCGCACACAGGGCGGGCAAGACGCCCTTCAA 63
 QY 44 ILECYSLARGASHISILEMETASPLEUCYSILEGLUCYSGLNAlaAsnGlnAlaSerAla 63
 Db 124 ATCTGAGGAAACCATATTGATGATCTTCATAGATGTCAGGCCAACCGAGGCTCCCT 183
 QY 64 THR SER GLU CYSTH VAL ALA TRP GLY VAL CYS ASN HIS ALA PHE HIS GLY HIS 83
 Db 184 ACTCTGAGAGCTGACCGTGGCGCTGTAACCAAGCTTCACTTCACCTTCACG 243
 QY 84 ILE SER ARG TRP LEU LYS THR ARG GLY VAL CYS PRO LEU ASP ASN ARG GLU TRP GLU 103
 Db 244 ATCTCTCGCTGCTCAAACACAGCAGGTGTCGGACACAGAGCTGGAAATC 303
 QY 104 GLU LYS ARG GLY HIS 108

Db 304 CAAGGTTGGCAC 318

RESULT 4

US-10-205-823-382/C

; Sequence 382, Application US/10205823

GENERAL INFORMATION:

; Publication No. US20030108963A1

; Sequence 20, Application US/09770791

; Patent No. US20030062014A1

GENERAL INFORMATION:

; Application: Schlegel, Robert

; Applicant: Monahan, John E.

; Applicant: Endge, Wilson O.

; Applicant: Gorbatcheva, Bella

; Applicant: Hoersch, Sebastian

; Applicant: Kamatkar, Shubhangi

; Applicant: Wonsey, Angela M.

; Applicant: Glatt, Karen

; Applicant: Zhao, Xumei

; Applicant: Anderson, Dustin

; Title of Invention: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF PROSTATE CANCER

; File Reference: MRI-044

CURRENT APPLICATION NUMBER: US/10/205-823

CURRENT FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307, 982

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: 60/314, 356

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/325, 020

PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/341, 746

PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: 60/362, 158

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 382

LENGTH: 511

TYPE: DNA

ORGANISM: Homo sapiens

US-10-205-823-382

Alignment Scores:

Pred. No.:	2.03e-65	Length:	511
Score:	554.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	89.94%	Indels:	0
DB:	14	Gaps:	0

US-09-541-462B-2 (1-108) x US-10-205-823-382 (1-511)

QY 3 AlalaMetAspValAspThrProSerGlyThrAsnSerIleAlaGlyLysIleArgPhe 22

Db 296 GCAAGCAGATGGATGCCAGGACACCACATGGCTTGTGCAAGTCAGCTAACCGCGTCC 237

QY 23 GluValLysLysIlePasnAlaValAlaLeutPAlaTrpAspIleValValAspnsCys 42

Db 236 GAAGTGAAGAAGTGGATGCCAGTACGCCCTCTGGCCTGGATAITGGTGTGAACTGTG 177

QY 43 AlatIleCysArgAsnHisIleMetAspLeuCysIleGlycylGluValCysAsnHisAlaPheHisPheHis 82

Db 116 GCTACTTCAGAAGAGTGACTGTCGATGGGGAGCTGTGAACTGCTTTCACCTCCAC 57

QY 83 CysteSerArgTrpLeuIsthrArgGlnValCysProLeuAspAspnsArgLys 100

Db 176 GCCACAGTCGCAAGAACACANTATGGCTTGTGCAAGTCAGCTAACCGCGTCC 117

QY 63 AlathSerGluGlyCysthValAlaTrpGlyValCysAsnHisAlaPheHisPheHis 82

QY 50 MetAspLeuCysIleGluCysGlnAlaAspGlnAlaSerAlaThrSerGlyGluCysThr 69

Db 200 ATGGATCTTGTGATTCGAGTGTGCAAGTCAGCTAACCGCGTCC 259

QY 70 ValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLys 89

Db 260 GTAGCCCGTGTGGCTTCTCAAACAAAGAAAGCTTAAGCCTTCACTGCATCACAGAGGCTAAAG 319

QY 90 ThrArgGlnValCysProLeuAspAspnsArgLysIleGluTrpGlyIleGlnLysTyrGlyHis 108

Db 320 ACTCGTCAAGTGTGTCATGGATAAGTGTGAGTGGAGTGTGCAAGANATAATGGTCAC 376

RESULT 6
US-09-780-016-27
Sequence 27, Application US/09780016
; Parent No. US2002004591A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. US2002004591A1el Human Proteases and
; FILE REFERENCE: LEX-012-USA
; CURRENT APPLICATION NUMBER: US/09/780-016
; CURRENT FILING DATE: 2001-02-09
; PRIORITY APPLICATION NUMBER: US 60/181,294
; PRIORITY FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-780-016-27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
; Alignment scores:
; Pred. No.: 1.79e-58 Length: 3208
; Score: 501.50 Matches: 88
; Percent Similarity: 95.70% Conservative: 1
; Best Local Similarity: 94.62% Mismatches: 1
; Query Match: 81.41% Indels: 3
; DB: Gaps: 1
; US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)
; Qy 16 GlyAlaGlyLysLysArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrp 35
; Db 2752 GGAGCTAAAAAAAAA-----AAAAATGGATGCACTGGCCTCTGGCCGG 2802
; Qy 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleIu 55
; Db 2803 GATATCTGGTGATAACTGTCGCACTGGCCTCTGGCCGG 2862
; Qy 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGlyCystIvalAlaTrpGlyCys 75
; Db 2863 TGTCAGCTAACCCAGGGTCCGTACITCAGAGAGTCGATGGCATGGAGTCGT 2922
; Qy 76 AsnHisAlaPheIleHisPheIleCysIleSerArgTripletsThrArgGlnValCysPro 95
; Db 2923 AACCATGCTTTCACTTCACCTTCACATCTCTGCTGGCTCAAAACACGGACAG 2982
; Qy 96 LeuAspAsnAsnGluLrpGluPheGlnLysTyrGlyHis 108
; Db 2983 TTGGCACACAGAGAGCTGGGATTCCAAGATGGGCAC 3021
; RESULT 8
US-09-918-995-1471
; Sequence 1471, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIORITY APPLICATION NUMBER: US/09/235,076
; PRIORITY FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 1471
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-918-995-1471
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; Alignment scores:
; Pred. No.: 3.69e-45 Length: 439
; Score: 396.00 Matches: 67
; Percent Similarity: 98.55% Conservative: 1
; Best Local Similarity: 97.10% Mismatches: 1
; Query Match: 64.29% Indels: 0
; DB: Gaps: 11

RESULT 7
US-10-214-811-27
; Sequence 27, Application US/10214811
; Publication No. US2003002302A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. US20030023062A1el Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/214,811

